Jesper N Tegner

List of Publications by Year
in descending order

188 papers	10,213 citations	71004 43 h-index	45040 94 g-index
212 all docs	212 docs citations	212 times ranked	19915 citing authors

#	Article	IF	Citations
1	Non-local Attention Improves Description Generation for Retinal Images. , 2022, , .		4
2	Deep neural network prediction of genome-wide transcriptome signatures â€" beyond the Black-box. Npj Systems Biology and Applications, 2022, 8, 9.	1.4	10
3	Deconvolution of the hematopoietic stem cell microenvironment reveals a high degree of specialization and conservation. IScience, 2022, 25, 104225.	1.9	2
4	Data-driven bioinformatics to disentangle cells within a tissue microenvironment. Trends in Cell Biology, 2022, 32, 467-469.	3.6	1
5	DeepOpht: Medical Report Generation for Retinal Images via Deep Models and Visual Explanation. , 2021, , .		24
6	A robust machine learning framework to identify signatures for frailty: a nested case-control study in four aging European cohorts. GeroScience, 2021, 43, 1317-1329.	2.1	31
7	STATegra: Multi-Omics Data Integration â€" A Conceptual Scheme With a Bioinformatics Pipeline. Frontiers in Genetics, 2021, 12, 620453.	1.1	24
8	DeepViral: prediction of novel virusâ€"host interactions from protein sequences and infectious disease phenotypes. Bioinformatics, 2021, 37, 2722-2729.	1.8	35
9	Predicting anti-PD-1 responders in malignant melanoma from the frequency of S100A9+ monocytes in the blood. , 2021, 9, e002171.		12
10	Gene Regulatory Network of Human GM-CSF-Secreting T Helper Cells. Journal of Immunology Research, 2021, 2021, 1-24.	0.9	2
11	Estimations of Integrated Information Based on Algorithmic Complexity and Dynamic Querying. , 2021, , 171-219.		0
12	DNA Transposon Expansion is Associated with Genome Size Increase in Mudminnows. Genome Biology and Evolution, 2021, 13, .	1.1	7
13	Deep characterization of paired chromatin and transcriptomes in four immune cell types from multiple sclerosis patients. Epigenomics, 2021, 13, 1607-1618.	1.0	4
14	VLG-Net: Video-Language Graph Matching Network for Video Grounding. , 2021, , .		23
15	Deep Deconvolution of the Hematopoietic Stem Cell Regulatory Microenvironment Reveals a High Degree of Specialization and Conservation between Mouse and Human. Blood, 2021, 138, 2168-2168.	0.6	0
16	MYC as a driver of stochastic chromatin networks: implications for the fitness of cancer cells. Nucleic Acids Research, 2020, 48, 10867-10876.	6.5	5
17	Evolving Neural Networks through a Reverse Encoding Tree. , 2020, , .		4
18	Elucidating the Role of Virulence Traits in the Survival of Pathogenic E. coli PI-7 Following Disinfection. Frontiers in Bioengineering and Biotechnology, 2020, 8, 614186.	2.0	0

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19	NLRP3 inflammasome activation regulates microglial migration. Alzheimer's and Dementia, 2020, 16, e040946.	0.4	0
20	Harmonization of quality metrics and power calculation in multi-omic studies. Nature Communications, 2020, 11, 3092.	5.8	43
21	Immunometabolic Network Interactions of the Kynurenine Pathway in Cutaneous Malignant Melanoma. Frontiers in Oncology, 2020, 10, 51.	1.3	5
22	Deriving disease modules from the compressed transcriptional space embedded in a deep autoencoder. Nature Communications, 2020, 11, 856.	5.8	37
23	Interpretable Self-Attention Temporal Reasoning for Driving Behavior Understanding. , 2020, , .		9
24	Algorithmic Probability-Guided Machine Learning on Non-Differentiable Spaces. Frontiers in Artificial Intelligence, 2020, 3, 567356.	2.0	4
25	Algorithmic Information Dynamics. Scholarpedia Journal, 2020, 15, 53143.	0.3	10
26	Non-parametric combination analysis of multiple data types enables detection of novel regulatory mechanisms in T cells of multiple sclerosis patients. Scientific Reports, 2019, 9, 11996.	1.6	13
27	Exhaustion of CD4+ T-cells mediated by the Kynurenine Pathway in Melanoma. Scientific Reports, 2019, 9, 12150.	1.6	54
28	Associations of Plasma 3-Methylhistidine with Frailty Status in French Cohorts of the FRAILOMIC Initiative. Journal of Clinical Medicine, 2019, 8, 1010.	1.0	25
29	Synthesizing New Retinal Symptom Images by Multiple Generative Models. Lecture Notes in Computer Science, 2019, , 235-250.	1.0	6
30	Auto-classification of Retinal Diseases in the Limit of Sparse Data Using a Two-Streams Machine Learning Model. Lecture Notes in Computer Science, 2019, , 323-338.	1.0	2
31	STATegra, a comprehensive multi-omics dataset of B-cell differentiation in mouse. Scientific Data, 2019, 6, 256.	2.4	26
32	Building gene regulatory networks from scATAC-seq and scRNA-seq using Linked Self Organizing Maps. PLoS Computational Biology, 2019, 15, e1006555.	1.5	56
33	Challenges in the Multivariate Analysis of Mass Cytometry Data: The Effect of Randomization. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2019, 95, 1178-1190.	1.1	12
34	An Algorithmic Information Calculus for Causal Discovery and Reprogramming Systems. IScience, 2019, 19, 1160-1172.	1.9	37
35	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. Nature Communications, 2019, 10, 2674.	5.8	240
36	The Thermodynamics of Network Coding, and an Algorithmic Refinement of the Principle of Maximum Entropy. Entropy, 2019, 21, 560.	1.1	8

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37	Neuronal methylome reveals CREB-associated neuro-axonal impairment in multiple sclerosis. Clinical Epigenetics, 2019, 11, 86.	1.8	24
38	MAPK pathway and B cells overactivation in multiple sclerosis revealed by phosphoproteomics and genomic analysis. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 9671-9676.	3.3	42
39	Combining evidence from four immune cell types identifies DNA methylation patterns that implicate functionally distinct pathways during Multiple Sclerosis progression. EBioMedicine, 2019, 43, 411-423.	2.7	45
40	Phosphatase inhibitor PPP1R11 modulates resistance of human T cells toward Treg-mediated suppression of cytokine expression. Journal of Leukocyte Biology, 2019, 106, 413-430.	1.5	17
41	Feedforward regulation of Myc coordinates lineage-specific with housekeeping gene expression during B cell progenitor cell differentiation. PLoS Biology, 2019, 17, e2006506.	2.6	8
42	TcellSubC: An Atlas of the Subcellular Proteome of Human T Cells. Frontiers in Immunology, 2019, 10, 2708.	2.2	14
43	Causal deconvolution by algorithmic generative models. Nature Machine Intelligence, 2019, 1, 58-66.	8.3	52
44	Algorithmic Information Dynamics of Emergent, Persistent, and Colliding Particles in the Game of Life *. , 2019, , 367-384.		2
45	Impact of genetic risk loci for multiple sclerosis on expression of proximal genes in patients. Human Molecular Genetics, 2018, 27, 912-928.	1.4	41
46	Hypermethylation of <i>MIR21</i> in CD4+ T cells from patients with relapsing-remitting multiple sclerosis associates with lower miRNA-21 levels and concomitant up-regulation of its target genes. Multiple Sclerosis Journal, 2018, 24, 1288-1300.	1.4	33
47	Symmetry and Correspondence of Algorithmic Complexity over Geometric, Spatial and Topological Representations. Entropy, 2018, 20, 534.	1.1	4
48	A Decomposition Method for Global Evaluation of Shannon Entropy and Local Estimations of Algorithmic Complexity. Entropy, 2018, 20, 605.	1.1	55
49	Algorithmic Complexity and Reprogrammability of Chemical Structure Networks. Parallel Processing Letters, 2018, 28, 1850005.	0.4	6
50	Predictive Systems Toxicology. Methods in Molecular Biology, 2018, 1800, 535-557.	0.4	4
51	Overexpression of endothelin B receptor in glioblastoma: a prognostic marker and therapeutic target?. BMC Cancer, 2018, 18, 154.	1.1	17
52	Time-resolved transcriptome and proteome landscape of human regulatory T cell (Treg) differentiation reveals novel regulators of FOXP3. BMC Biology, 2018, 16, 47.	1.7	23
53	A Review of Graph and Network Complexity from an Algorithmic Information Perspective. Entropy, 2018, 20, 551.	1.1	47
54	DNA methylation as a mediator of HLA-DRB1*15:01 and a protective variant in multiple sclerosis. Nature Communications, 2018, 9, 2397.	5.8	147

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55	Functional genomics analysis of vitamin D effects on CD4+ T cells in vivo in experimental autoimmune encephalomyelitis â€¬. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1678-E1687.	3.3	81
56	Comment on â€œEpigenetics in the pathogenesis of RAâ€¢ Seminars in Immunopathology, 2017, 39, 421-422.	2.8	0
57	SCENERY: a web application for (causal) network reconstruction from cytometry data. Nucleic Acids Research, 2017, 45, W270-W275.	6.5	9
58	A minimal unified model of disease trajectories captures hallmarks of multiple sclerosis. Mathematical Biosciences, 2017, 289, 1-8.	0.9	8
59	Predicting Causal Relationships from Biological Data: Applying Automated Causal Discovery on Mass Cytometry Data of Human Immune Cells. Scientific Reports, 2017, 7, 12724.	1.6	21
60	Guidelines for Developing Successful Short Advanced Courses in Systems Medicine and Systems Biology. Cell Systems, 2017, 5, 168-175.	2.9	7
61	Low-algorithmic-complexity entropy-deceiving graphs. Physical Review E, 2017, 96, 012308.	0.8	47
62	HiDi: an efficient reverse engineering schema for large-scale dynamic regulatory network reconstruction using adaptive differentiation. Bioinformatics, 2017, 33, 3964-3972.	1.8	11
63	Viva Europa, a Land of Excellence in Research and Innovation for Health and Wellbeing. Progress in Preventive Medicine (New York, N Y), 2017, 2, e006.	0.7	6
64	Iterative Systems Biology for Medicine â€“ Time for advancing from network signatures to mechanistic equations. Current Opinion in Systems Biology, 2017, 3, 111-118.	1.3	4
65	Phosphoproteomics Reveals Regulatory T Cell-Mediated DEF6 Dephosphorylation That Affects Cytokine Expression in Human Conventional T Cells. Frontiers in Immunology, 2017, 8, 1163.	2.2	13
66	Dynamics and heterogeneity of brain damage in multiple sclerosis. PLoS Computational Biology, 2017, 13, e1005757.	1.5	33
67	Systems Toxicology: Systematic Approach to Predict Toxicity. Current Pharmaceutical Design, 2017, 22, 6911-6917.	0.9	7
68	The Information-Theoretic and Algorithmic Approach to Human, Animal, and Artificial Cognition. Studies in Applied Philosophy, Epistemology and Rational Ethics, 2017, , 117-139.	0.2	4
69	TGF-Î² Affects the Differentiation of Human GM-CSF+ CD4+ T Cells in an Activation- and Sodium-Dependent Manner. Frontiers in Immunology, 2016, 7, 603.	2.2	6
70	Proposals for enhanced health risk assessment and stratification in an integrated care scenario. BMJ Open, 2016, 6, e010301.	0.8	61
71	A perspective on bridging scales and design of models using low-dimensional manifolds and data-driven model inference. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2016, 374, 20160144.	1.6	14
72	Adaptive input data transformation for improved network reconstruction with information theoretic algorithms. Statistical Applications in Genetics and Molecular Biology, 2016, 15, 507-520.	0.2	0

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73	From comorbidities of chronic obstructive pulmonary disease to identification of shared molecular mechanisms by data integration. BMC Bioinformatics, 2016, 17, 441.	1.2	20
74	High-specificity bioinformatics framework for epigenomic profiling of discordant twins reveals specific and shared markers for ACPA and ACPA-positive rheumatoid arthritis. Genome Medicine, 2016, 8, 124.	3.6	27
75	Human macrophages induce CD4⁺Foxp3⁺ regulatory T cells via binding and reâ€release of TGFâ€l². Immunology and Cell Biology, 2016, 94, 747-762.	1.0	85
76	Conditional Disease Development extracted from Longitudinal Health Care Cohort Data using Layered Network Construction. Scientific Reports, 2016, 6, 26170.	1.6	15
77	In Vitro Differentiation of Human CD4<sup>+</sup>FOXP3<sup>+</sup> Induced Regulatory T Cells (iTregs) from Na&#239;ve CD4<sup>+</sup> T Cells Using a TGF-&#946;-containing Protocol. Journal of Visualized Experiments, 2016, , .	0.2	11
78	Methods of information theory and algorithmic complexity for network biology. Seminars in Cell and Developmental Biology, 2016, 51, 32-43.	2.3	40
79	Computational Modeling Under Uncertainty: Challenges and Opportunities. Studies in Mechanobiology, Tissue Engineering and Biomaterials, 2016, , 467-476.	0.7	3
80	Modeling and Model Simplification to Facilitate Biological Insights and Predictions. Studies in Mechanobiology, Tissue Engineering and Biomaterials, 2016, , 301-325.	0.7	6
81	Probabilistic Computational Causal Discovery for Systems Biology. Studies in Mechanobiology, Tissue Engineering and Biomaterials, 2016, , 33-73.	0.7	27
82	Evaluating network inference methods in terms of their ability to preserve the topology and complexity of genetic networks. Seminars in Cell and Developmental Biology, 2016, 51, 44-52.	2.3	28
83	Quantifying loss of information in network-based dimensionality reduction techniques. Journal of Complex Networks, 2016, 4, 342-362.	1.1	16
84	Normalization of circulating microRNA expression data obtained by quantitative real-time RT-PCR. Briefings in Bioinformatics, 2016, 17, 204-212.	3.2	211
85	Optimization in Biology Parameter Estimation and the Associated Optimization Problem. Studies in Mechanobiology, Tissue Engineering and Biomaterials, 2016, , 177-197.	0.7	17
86	In Search of â€˜Omics'-Based Biomarkers to Predict Risk of Frailty and Its Consequences in Older Individuals: The FRAILOMIC Initiative. Gerontology, 2016, 62, 182-190.	1.4	69
87	From Systems Understanding to Personalized Medicine: Lessons and Recommendations Based on a Multidisciplinary and Translational Analysis of COPD. Methods in Molecular Biology, 2016, 1386, 283-303.	0.4	10
88	Comparative Analysis of Protocols to Induce Human CD4+Foxp3+ Regulatory T Cells by Combinations of IL-2, TGF-beta, Retinoic Acid, Rapamycin and Butyrate. PLoS ONE, 2016, 11, e0148474.	1.1	89
89	<i>Human cytomegalovirus</i> may promote tumour progression by upregulating arginase-2. Oncotarget, 2016, 7, 47221-47231.	0.8	18
90	Health risk assessment and stratification in an integrated care scenario. International Journal of Integrated Care, 2016, 16, 322.	0.1	3

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91	IL-1β promotes Th17 differentiation by inducing alternative splicing of FOXP3. Scientific Reports, 2015, 5, 14674.	1.6	96
92	The folate-coupled enzyme MTHFD2 is a nuclear protein and promotes cell proliferation. Scientific Reports, 2015, 5, 15029.	1.6	85
93	Bioinformatics Mining and Modeling Methods for the Identification of Disease Mechanisms in Neurodegenerative Disorders. International Journal of Molecular Sciences, 2015, 16, 29179-29206.	1.8	47
94	Introduction to Data Types in Epigenomics. Translational Bioinformatics, 2015, , 3-34.	0.0	2
95	VEGF-B promotes cancer metastasis through a VEGF-A–independent mechanism and serves as a marker of poor prognosis for cancer patients. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E2900-9.	3.3	112
96	Laboratory biomarkers and frailty: presentation of the FRAILOMIC initiative. Clinical Chemistry and Laboratory Medicine, 2015, 53, e253-5.	1.4	17
97	Topological Evaluation of Methods for Reconstruction of Genetic Regulatory Networks. , 2015, , .		0
98	Monozygotic twins discordant for common variable immunodeficiency reveal impaired DNA demethylation during naïve-to-memory B-cell transition. Nature Communications, 2015, 6, 7335.	5.8	81
99	Signaling networks in MS: A systems-based approach to developing new pharmacological therapies. Multiple Sclerosis Journal, 2015, 21, 138-146.	1.4	24
100	Numerical Investigation of Graph Spectra and Information Interpretability of Eigenvalues. Lecture Notes in Computer Science, 2015, , 395-405.	1.0	2
101	An integrative analysis reveals coordinated reprogramming of the epigenome and the transcriptome in human skeletal muscle after training. Epigenetics, 2014, 9, 1557-1569.	1.3	184
102	Breast Cancer MicroRNAs: Clinical Biomarkers for the Diagnosis and Treatment Strategies. , 2014, , 171-182.		3
103	Non-HLA genes PTPN22, CDK6 and PADI4 are associated with specific autoantibodies in HLA-defined subgroups of rheumatoid arthritis. Arthritis Research and Therapy, 2014, 16, 414.	1.6	23
104	Methylome characterization of CD4+ T cells in multiple sclerosis – Establishing a role for miR-21 in autoimmune disease. Journal of Neuroimmunology, 2014, 275, 112.	1.1	0
105	Data integration in the era of omics: current and future challenges. BMC Systems Biology, 2014, 8, I1.	3.0	300
106	STATegra EMS: an Experiment Management System for complex next-generation omics experiments. BMC Systems Biology, 2014, 8, S9.	3.0	19
107	Systems Medicine: from molecular features and models to the clinic in COPD. Journal of Translational Medicine, 2014, 12, S4.	1.8	23
108	Chronic Obstructive Pulmonary Disease heterogeneity: challenges for health risk assessment, stratification and management. Journal of Translational Medicine, 2014, 12, S3.	1.8	34

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109	Biomedical research in a Digital Health Framework. Journal of Translational Medicine, 2014, 12, S10.	1.8	21
110	Predictive medicine: outcomes, challenges and opportunities in the Synergy-COPD project. Journal of Translational Medicine, 2014, 12, S12.	1.8	6
111	Synergy-COPD: a systems approach for understanding and managing chronic diseases. Journal of Translational Medicine, 2014, 12, S2.	1.8	19
112	Accelerating Translational Research by Clinically Driven Development of an Informatics Platform—A Case Study. PLoS ONE, 2014, 9, e104382.	1.1	10
113	Oxygen Pathway Modeling Estimates High Reactive Oxygen Species Production above the Highest Permanent Human Habitation. PLoS ONE, 2014, 9, e111068.	1.1	14
114	Network Biology Empowering Detection and Understanding of Interactions Between Genetic Factors in Development of Complex Phenotypes. , 2014, , 175-194.		0
115	Implementation of the CDC translational informatics platform - from genetic variants to the national Swedish Rheumatology Quality Register. Journal of Translational Medicine, 2013, 11, 85.	1.8	8
116	Identification of novel markers in rheumatoid arthritis through integrated analysis of DNA methylation and microRNA expression. Journal of Autoimmunity, 2013, 41, 6-16.	3.0	144
117	A vision and strategy for the virtual physiological human: 2012 update. Interface Focus, 2013, 3, 20130004.	1.5	74
118	Integrative approaches to computational biomedicine. Interface Focus, 2013, 3, 20130003.	1.5	10
119	Pediatric systems medicine: evaluating needs and opportunities using congenital heart block as a case study. Pediatric Research, 2013, 73, 508-513.	1.1	8
120	A beta-mixture quantile normalization method for correcting probe design bias in Illumina Infinium 450 k DNA methylation data. Bioinformatics, 2013, 29, 189-196.	1.8	1,295
121	An evaluation of analysis pipelines for DNA methylation profiling using the Illumina HumanMethylation450 BeadChip platform. Epigenetics, 2013, 8, 333-346.	1.3	192
122	Algorithmic complexity of motifs clusters superfamilies of networks. , 2013, , .		4
123	Pre-B cell to macrophage transdifferentiation without significant promoter DNA methylation changes. Nucleic Acids Research, 2012, 40, 1954-1968.	6.5	37
124	Systems medicine and integrated care to combat chronic noncommunicable diseases. Genome Medicine, 2011, 3, 43.	3.6	181
125	Blood levels of dual-specificity phosphatase-1 independently predict risk for post-operative morbidities causing prolonged hospitalization after coronary artery bypass grafting. International Journal of Molecular Medicine, 2011, 27, 851-7.	1.8	4
126	Epigenetic alterations in autoimmune disease. Journal of Translational Medicine, 2011, 9, .	1.8	1

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127	Decoding complex biological networks - tracing essential and modulatory parameters in complex and simplified models of the cell cycle. BMC Systems Biology, 2011, 5, 123.	3.0	8
128	Workflow for generating competing hypothesis from models with parameter uncertainty. Interface Focus, 2011, 1, 438-449.	1.5	33
129	ParkDB: a Parkinson's disease gene expression database. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar007-bar007.	1.4	28
130	Non-HLA-DRB1 RA-associated risk alleles associate with anti-CCP and specific ACPA levels. Annals of the Rheumatic Diseases, 2011, 70, A20-A21.	0.5	0
131	Carotid Plaque Age Is a Feature of Plaque Stability Inversely Related to Levels of Plasma Insulin. PLoS ONE, 2011, 6, e18248.	1.1	18
132	A vision and strategy for the virtual physiological human in 2010 and beyond. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2010, 368, 2595-2614.	1.6	136
133	DGAT1 Participates in the Effect of <i>HNF4A</i> on Hepatic Secretion of Triglyceride-Rich Lipoproteins. Arteriosclerosis, Thrombosis, and Vascular Biology, 2010, 30, 962-967.	1.1	14
134	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. Cell, 2010, 140, 744-752.	13.5	667
135	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. Cell, 2010, 141, 369.	13.5	4
136	Mechanism for top-down control of working memory capacity. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 6802-6807.	3.3	305
137	Multi-Organ Expression Profiling Uncovers a Gene Module in Coronary Artery Disease Involving Transendothelial Migration of Leukocytes and LIM Domain Binding 2: The Stockholm Atherosclerosis Gene Expression (STAGE) Study. PLoS Genetics, 2009, 5, e1000754.	1.5	118
138	On reliable discovery of molecular signatures. BMC Bioinformatics, 2009, 10, 38.	1.2	30
139	Computational disease modeling â€" fact or fiction?. BMC Systems Biology, 2009, 3, 56.	3.0	41
140	Can modular analysis identify disease-associated candidate genes for therapeutics?. Journal of Biology, 2009, 8, 48.	2.7	1
141	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. Nature Genetics, 2009, 41, 553-562.	9.4	408
142	Reverse Engineering of Gene Networks with LASSO and Nonlinear Basis Functions. Annals of the New York Academy of Sciences, 2009, 1158, 265-275.	1.8	27
143	Bridging the gap between systems biology and medicine. Genome Medicine, 2009, 1, 88.	3.6	61
144	Transcription Regulatory Networks Analysis Using CAGE. , 2009, , 153-168.		0

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145	Integrated approaches to uncovering transcription regulatory networks in mammalian cells. Genomics, 2008, 91, 219-231.	1.3	38
146	Electrotonic Signals along Intracellular Membranes May Interconnect Dendritic Spines and Nucleus. PLoS Computational Biology, 2008, 4, e1000036.	1.5	20
147	Transcriptional Profiling Uncovers a Network of Cholesterol-Responsive Atherosclerosis Target Genes. PLoS Genetics, 2008, 4, e1000036.	1.5	67
148	ApoB100-LDL Acts as a Metabolic Signal from Liver to Peripheral Fat Causing Inhibition of Lipolysis in Adipocytes. PLoS ONE, 2008, 3, e3771.	1.1	23
149	Evidence of Highly Regulated Genes (in-Hubs) in Gene Networks of Saccharomyces Cerevisiae. Bioinformatics and Biology Insights, 2008, 2, BBI.S853.	1.0	1
150	Human C-reactive protein slows atherosclerosis development in a mouse model with human-like hypercholesterolemia. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 13768-13773.	3.3	110
151	Thematic review series: Systems Biology Approaches to Metabolic and Cardiovascular Disorders. Multi-organ whole-genome measurements and reverse engineering to uncover gene networks underlying complex traits. Journal of Lipid Research, 2007, 48, 267-277.	2.0	19
152	Stronger Synaptic Connectivity as a Mechanism behind Development of Working Memory-related Brain Activity during Childhood. Journal of Cognitive Neuroscience, 2007, 19, 750-760.	1.1	103
153	FRONTO-PARIETAL CONNECTION ASYMMETRY REGULATES WORKING MEMORY DISTRACTIBILITY. Journal of Integrative Neuroscience, 2007, 06, 567-596.	0.8	16
154	Towards scalable and data efficient learning of Markov boundaries. International Journal of Approximate Reasoning, 2007, 45, 211-232.	1.9	148
155	Detecting multivariate differentially expressed genes. BMC Bioinformatics, 2007, 8, 150.	1.2	28
156	Perturbations to uncover gene networks. Trends in Genetics, 2007, 23, 34-41.	2.9	51
157	Neuronal firing rates account for distractor effects on mnemonic accuracy in a visuo-spatial working memory task. Biological Cybernetics, 2007, 96, 407-419.	0.6	17
158	Learning and Validating Bayesian Network Models of Gene Networks. Studies in Fuzziness and Soft Computing, 2007, , 359-375.	0.6	3
159	Transcriptional network dynamics in macrophage activation. Genomics, 2006, 88, 133-142.	1.3	125
160	Systems biology of innate immunity. Cellular Immunology, 2006, 244, 105-109.	1.4	35
161	Detection of compound mode of action by computational integration of whole-genome measurements and genetic perturbations. BMC Bioinformatics, 2006, 7, 51.	1.2	16
162	Brain Activity Related to Working Memory and Distraction in Children and Adults. Cerebral Cortex, 2006, 17, 1047-1054.	1.6	150

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163	Evaluating Feature Selection for SVMs in High Dimensions. Lecture Notes in Computer Science, 2006, , 719-726.	1.0	13
164	Scalable, Efficient and Correct Learning of Markov Boundaries Under the Faithfulness Assumption. Lecture Notes in Computer Science, 2005, , 136-147.	1.0	12
165	Learning dynamic Bayesian network models via cross-validation. Pattern Recognition Letters, 2005, 26, 2295-2308.	2.6	23
166	Systems Biology Is Taking Off. Genome Research, 2003, 13, 2377-2380.	2.4	36
167	Temporally Irregular Mnemonic Persistent Activity in Prefrontal Neurons of Monkeys During a Delayed Response Task. Journal of Neurophysiology, 2003, 90, 3441-3454.	0.9	235
168	The Logic of Life. Genome Research, 2003, 13, 2375-2376.	2.4	0
169	Reverse engineering gene networks: Integrating genetic perturbations with dynamical modeling. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 5944-5949.	3.3	380
170	Reverse engineering gene networks using singular value decomposition and robust regression. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 6163-6168.	3.3	582
171	An adaptive spike-timing-dependent plasticity rule. Neurocomputing, 2002, 44-46, 189-194.	3.5	3
172	Spike-timing-dependent plasticity: common themes and divergent vistas. Biological Cybernetics, 2002, 87, 446-458.	0.6	89
173	The dynamical stability of reverberatory neural circuits. Biological Cybernetics, 2002, 87, 471-481.	0.6	130
174	GABAB-ergic modulation of burst rate and intersegmental coordination in lamprey: experiments and simulations. Brain Research, 2000, 864, 81-86.	1.1	8
175	Interactive Effects of the GABABergic Modulation of Calcium Channels and Calcium-Dependent Potassium Channels in Lamprey. Journal of Neurophysiology, 1999, 81, 1318-1329.	0.9	17
176	The synaptic NMDA component desynchronizes neural bursters. Neurocomputing, 1999, 26-27, 557-563.	3.5	0
177	Control of burst proportion and frequency range by drive-dependent modulation of adaptation. Neurocomputing, 1999, 26-27, 185-191.	3.5	1
178	Modulation of burst frequency by calcium-dependent potassium channels in the lamprey locomotor system: dependence of the activity level. Journal of Computational Neuroscience, 1998, 5, 121-140.	0.6	30
179	Intrinsic function of a neuronal network â€" a vertebrate central pattern generator. Brain Research Reviews, 1998, 26, 184-197.	9.1	217
180	Activity Dependent Modulation of the Burst Rate by Calcium-Dependent Potassium Channels in Lamprey. , 1998, , 549-554.		3

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181	Modulation of Oscillatory Properties, Burst Rates, Intersegmental Coordination By Gabab- Receptor Activation in the Lamprey. , 1998, , 543-548.		0
182	Low-Voltage-Activated Calcium Channels in the Lamprey Locomotor Network: Simulation and Experiment. Journal of Neurophysiology, 1997, 77, 1795-1812.	0.9	53
183	A Computational and Experimental Study of Rebound Firing and Modulatory Effects on the Lamprey Spinal Network. , 1997, , 519-524.		1
184	Causality, Information, and Biological Computation: An Algorithmic Software Approach to Life, Disease, and the Immune System. , 0, , 244-280.		6
185	COVID-19 and beyond:Âa call for action andÂaudacious solidarity to all the citizens and nations,Âit is humanityâ€™s fight. F1000Research, 0, 9, 1130.	0.8	3
186	Testing Biological Models for Non-linear Sensitivity with a Programmability Test. , 0, , .		2
187	COVID-19 and Beyond: A Call for Action and Audacious Solidarity to All the Citizens and Nations, It Is Humanityâ€™s Fight. SSRN Electronic Journal, 0, , .	0.4	1
188	Deep Deconvolution of the Hematopoietic Stem Cell Regulatory Microenvironment Reveals a High Degree of Specialization and Conservation Between Mouse and Human. SSRN Electronic Journal, 0, , .	0.4	0